

Notch (C)	IDE \bar{C} -SNP	\bar{C} QNGGTC---D-V \bar{G} SY- \bar{C} - \bar{C} PP \bar{G} FT	\bar{G} K--- \bar{C} E-N
<u>10244 (C)</u>	-NE \bar{C} TM---	\bar{C} QH--- \bar{C}	VNT- \bar{G} SY- \bar{C} K \bar{C} -S \bar{G} --
80			\bar{G} --L- \bar{C} D
95	VNE \bar{C} G \bar{M} KPRP	\bar{C} QHR \bar{C}	\bar{C} R \bar{C} FP \bar{G} YT
133	VNSRTCAMIN	\bar{C} QYS \bar{C}	\bar{G} KT \bar{C} SQ D
175	IDE \bar{C} ASGKVI	\bar{C} PYNRR \bar{C}	\bar{G} HMLMP D
220	INE \bar{C} TMDSHT	\bar{C} SHHAN \bar{C}	\bar{G} LRLAPN
			LQYISGR
			\bar{G} NGRL \bar{C} S
<u>CD97 (C)</u>	V-E \bar{C} -S \bar{G} -Q-- \bar{C} -SS-- \bar{C}	-NTV \bar{G} SY- \bar{C} R \bar{C} RP \bar{G} W-P-P \bar{G} -PN---	D
<u>EGF (C)</u>	NSDSE \bar{C} PLSHDGY \bar{C} LHDGV \bar{C} MYIEALDKYA \bar{C} N \bar{C} VV \bar{G} YI---	\bar{G} E-R-- \bar{C} QYRDLKWWELR	

Figure 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 SEQ ID NO: 1

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
 GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGACTCCGCC TGGCCCCAAA
 TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
 GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTACTGCAAA
 TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT
 AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
 ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
 AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
 AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
 CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA
 GAACCCACCA GGACTCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA
 TGAAGAGATA GTTTCAGAG GCGGGAAGT TCATGGAGGT AAAAAAGGGA
 ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
 GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
 CCCTAAGGTG AATGAAGCAG GTGAATTCTG CCTGATTCTG GTCCAAAGGA
 AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTTGAC
 TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
 TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
 CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAACTT
 CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
 CCGGCTGGCC GGAGACAAAG TCGGGAAGT TCGAGTGTTT GTGAAAAACA
 GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAGTGG
 AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CAAAAGCAT
 CATTTTTGAA GCAGAACGTG GCAAGGGCAA AACCGGCGAA ATCGCAGTGG
 ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG
 GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCT
 GGTTTTTTTT ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
 CTGAAAAATT G
 SEQ ID NO: 2

FIGURE 2

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
SEQ ID NO:3

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPKVNLPFNYYEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVGKLRVFKNSNNALAWKTTSEDEKWKTKGIQLYQGTDATKSIIF
EAERGKGKTGEIAVDGVLLVSGLCPDLSLSVDDXMVLSLYLTLYVSSLVFLILHHRTSGI
LKLLAEKL
SEQ ID NO:4

FIGURE 3

20220409 14:09:00

ACTAGTGATTCCATCCTAATACGACTCACTATAGGGCTCGAGCGCGCGCCCGGGCAGGTCGTGCAGGGACAGCACCCCGGTA
ACTCGAGTGGAGCGGAGGACCGGAGCGGCTGAGAGAGAGAGGCGCGGCTTAGCTGCTACGGGGTCGGCCGGCGCC
CTCCGAGGGGGCTCAGGAGGAGGAGGAGCCGTGCGAGAA TGCCCTTGCCCTGGAGCCTTGCGCTCCCGTCTGCT
CTCCCTGGGTGGCAGGTGGTTTCGGGAAACGGCGCCAGTGCAAGGCATCACGGGTGTGTAGCATCGGCACGTGACGCTGG
GGTCTGTCACTATGGAACTAATAACCTGGCCTGCTGCTACGGTGGAGAAAGAAACAGCAAGGGAGTCTGTGAAGCTACATGCG
AACCTGGATGTAAGTTGGTGAGTGGCGTGGGACCAACAAATCGAGATGCTTTCAGGATACACCGGGGAAAAACCTGCGAGT
CAAGATGTGAATGAGTGTGGAATGAAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAGAGCTACAAGTGCCT
TTGCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAAACTGTTCAGTATA
GCTGTGAAGACACAGAAAGGGCCACAGTGCCTGTGTCCATCTTCAGGACTCGCCCTGGCCCCAAATTTGGAAGGAGACTGT
CTAGATATTGATGAATGTGCCTCTGTGTAAGTCACTGTGCCATCAATCGAAGATGTGTGAACACATTTTGGAAAGCTACTA
CTGCAAAATGTCACATTTGGTTTCGAACCTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGG
ATAGCCATACGTGCAGCCACCATGCCAATTTGCTTCAATACCCCAAGGTCCTTCAAGTGTAAATGTAAGCAGGGATATAAA
GGCAATGGACTTCGGGTGTTCTGCTATCCCTGAAAAATCTGTGAAAGGAAGTCTCAGAGCACCTGGTACCATCAAGACAG
AATCAAGAAAGTTGCTGCTCACAAAAACAGCATGAAAAAGAAAGCAAAAAATATAAAAAATGTTACCCAGAACCCACAGCA
CTCCTACCCCTAAGGTGAACCTTGCGACCCCTTCAACTATGAAGAGATAGTTTCAGAGGCGGGAACCTCTCATGGAGGTAAA
AAAGGGAATGAACAGAAAAATGAAGAGGGGCTTGAGATGAGAAAGAGAAAGAGAAAGCCCTGAAGAAATGACWTAGAGGA
CGGAAAGCTCGCAGGAGATGTGTTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCGTGGTCCAAAGGAAAG
CGCTAACTTCCAAACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACTGGAAA
CAGGATAGAGAAGATGATTTTGACTGGAAATCCTGCTGATCGAGATAATGCTATTTGGCTTCTATATGGCAGCTTCCGGCCCTT
GGCAGGTACAAGAAAGACATTTGGCCGATTTGAAACTTCTCTACCTGACCTGCAACCCCAAGCAACTCTGTGTTGCTCT
TTGATTTACCGGTGGCCGAGACAAAAGTGGGAACTTCGAGTGTGTGTGAAAAACAGTAAACAAATGCCCCGGCATGGGAG
AAGACCACGAGTGGATGAAAGTGGAAAGACAGGAAAAATTCAGTTGTATCAAGGAACTGATGCTACCAAAAGCATCAT
TTTTTGAAGCAGAAACGTGGCAAGGGCAAAACCGGCGAAAATCGCAGTGGATGGCGCTTTGCTTGTTCAGGCTTATGTCCAG
ATAGCCTTTTATCTGTGATGATGAAATGTTACTATCTTTATATTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGATA
TTGSAATCATAGGACCTCTGGCATTTTAAAAATTAAGCTGAAAAATTTGTAATGTACCAACAGAAAAATTAATTTGTAAGA
TGCCCTTTMTTGTAATAAGATATGCCAAATATTTGGCTTTAAATATCATATCATCTGATCTTCTCAGTCAATTTCTGAATCTTTT
CACATTTATATTAATAATATGGAATGTCAGGTTTTATCTCCCTCCTCAGTATATCTGATTTGTATAGTAAGTAAGTTGATGA
GCTTCTCTGCAACATTTCTAGAAAAATAGAAAAAAGCAAGAGAAATGTTTAACTGTTTGACTCTTATGATAGATGTTTT
TGAAAACTATGACATCAAAAGATAGACTTTTGCCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAACTGTGATATTTAAAT
TCTTTGTAAATAATAATATCCAAATCATCAAAAAAATAAAAAA

SEQ ID NO: 5

FIGURE 4

**EGFL6 (221-260 aa)
3D Model**

**EGF
NMR Structure**

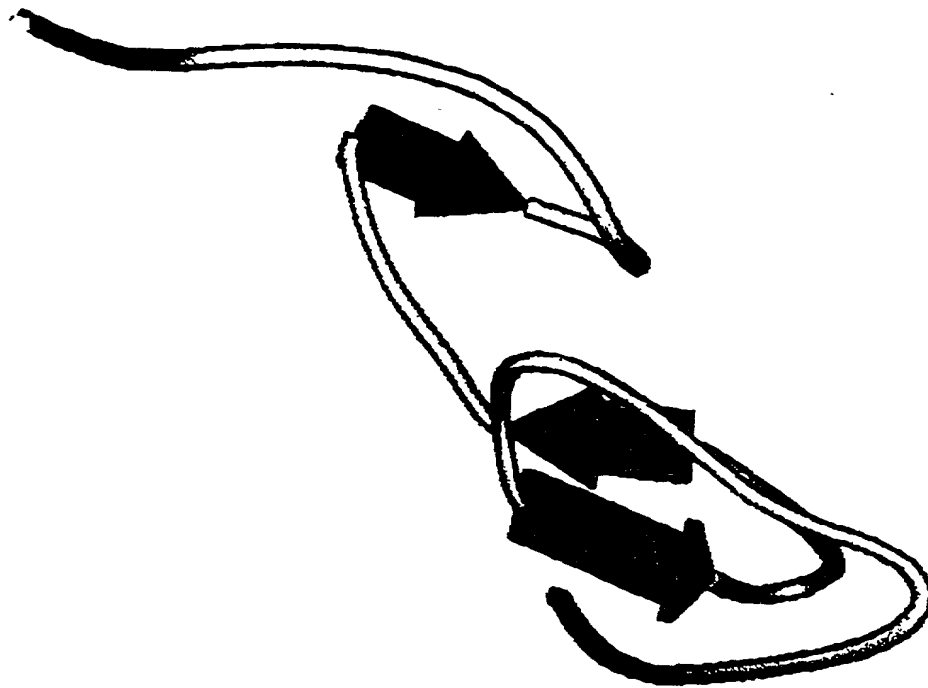
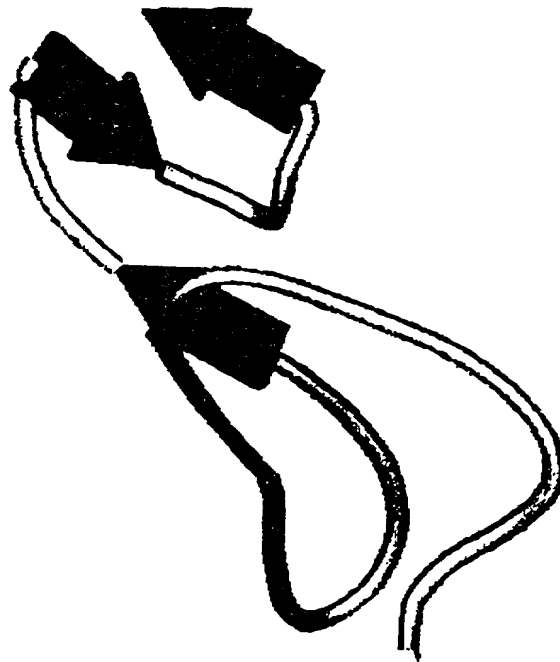


Figure 5